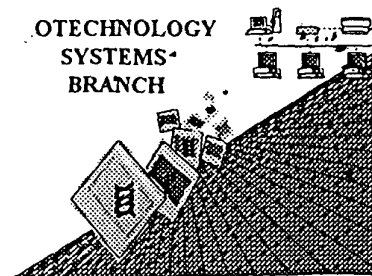


## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09 936 845

Source: PCT 09

Date Processed by STIC: 10 03 01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

PCT09

## RAW SEQUENCE LISTING

DATE: 10/03/2001

PATENT APPLICATION: US/09/936,845

TIME: 10:29:43

Input Set : A:\NAPIER PCT-GB00-01035 sequence listing.txt

Output Set: N:\CRF3\10032001\I936845.raw

3 <110> APPLICANT: Napier, Johnathan A.  
 5 <120> TITLE OF INVENTION: Polyunsaturated Fatty Acid (PUFA) Elongase from *Caenorhabditis elegans*  
 7 <130> FILE REFERENCE: 76/7  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/936,845  
 C--> 10 <141> CURRENT FILING DATE: 2001-09-18  
 12 <160> NUMBER OF SEQ ID NOS: 22  
 14 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply  
Corrected Diskette Needed

## ERRORED SEQUENCES

728 <210> SEQ ID NO: 22  
 729 <211> LENGTH: 269  
 730 <212> TYPE: PRT  
 731 <213> ORGANISM: C. elegans  
 733 <400> SEQUENCE: 22  
 734 Met Ser Ala Glu Val Ser Glu Arg Phe Lys Val Trp Thr Gly Asn Asn  
 735 1 5 10 15  
 737 Glu Thr Ile Ile Tyr Ser Pro Phe Glu Tyr Asp Ser Thr Leu Leu Ile  
 738 20 25 30  
 740 Glu Ser Cys Arg Cys Thr Tyr Gln Leu Leu Ile Leu Leu Arg Gln Ile  
 741 35 40 45  
 E--> 743 Tyr Tyr Arg Asp Ile Trp Ser His Gly Asn Leu Lys Ala Cys Asp Xaa  
 744 50 55 60  
 746 Leu Leu Leu Ala Trp Asn Gly Phe Leu Ala Val Phe Ser Ile Met Gly  
 747 65 70 75 80  
 E--> 749 Thr Trp Arg Phe Gly Ile Glu Phe Tyr Asp Ala Val Phe Arg Xaa Gly  
 750 85 90 95  
 E--> 752 Phe Ile Xaa Ser Ile Cys Leu Ala Val Asn Pro Arg Ser Pro Ser Ala  
 753 100 105 110  
 755 Phe Trp Ala Cys Met Phe Ala Leu Ser Lys Ile Ala Glu Phe Gly Asp  
 756 115 120 125  
 758 Thr Met Phe Leu Val Leu Arg Lys Arg Pro Val Ile Phe Leu His Trp  
 759 130 135 140  
 761 Tyr His His Ala Val Val Leu Ile Leu Ser Trp His Ala Ala Ile Glu  
 762 145 150 155 160  
 764 Leu Thr Ala Pro Gly Arg Trp Phe Ile Phe Met Asn Tyr Leu Val His  
 765 165 170 175  
 E--> 767 Ser Ile Met Tyr Thr Tyr Tyr Ala Ile Thr Ser Ile Gly Tyr Arg Xaa  
 768 180 185 190  
 770 Pro Lys Ile Val Ser Met Thr Val Thr Phe Leu Gln Thr Leu Gln Met  
 771 195 200 205  
 773 Leu Ile Gly Val Ser Ile Ser Cys Ile Val Leu Tyr Leu Lys Leu Asn  
 774 210 215 220  
 776 Gly Glu Met Cys Gln Gln Ser Tyr Asp Asn Leu Ala Leu Ser Phe Gly  
 777 225 230 235 240  
 779 Ile Tyr Ala Ser Phe Leu Val Leu Ser Ser Phe Phe Asn Asn Ala Tyr

*Must enumerate unknown proteins on  
 221, 222 and 223. Specifically,  
 you must specify a variant location  
 and values for Xaa*

## RAW SEQUENCE LISTING

DATE: 10/03/2001

PATENT APPLICATION: US/09/936,845

TIME: 10:29:43

Input Set : A:\NAPIER PCT-GB00-01035 sequence listing.txt

Output Set: N:\CRF3\10032001\I936845.raw

780		245		250		255							
782	Leu	Val	Lys	Lys	Asp	Lys	Lys	Pro	Asp	Val	Lys	Lys	Asp
783			260						265				

VERIFICATION SUMMARY

DATE: 10/03/2001

PATENT APPLICATION: US/09/936,845

TIME: 10:29:44

Input Set : A:\NAPIER PCT-GB00-01035 sequence listing.txt

Output Set: N:\CRF3\10032001\I936845.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:743 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22  
M:340 Repeated in SeqNo=22

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 091936845

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
<210> sequence id number  
<400> sequence id number  
000
- 9 ✓ Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.